Claims

1. A nucleic acid sequence comprising any one of the nucleic acid sequences of SEQ ID NOs 1-20, or a subfragment nucleic acid sequence derived from any one of the sequences of SEQ ID NOs 1-20, wherein an mRNA molecule comprising said sequence has RNA binding protein (RBP) binding activity or regulates the functionality of said mRNA.

2. The nucleic acid sequence of claim 1, wherein said subfragment nucleic acid sequence is optimized.

3. The nucleic acid sequence of claim 1, wherein the regulation of mRNA functionality comprises an alteration in pre-mRNA processing or in the stabilization, translational efficiency, localization, sequestration, editing, or splicing functions of said mRNA.

4. A method of identifying an optimized subfragment of any one of the parent nucleic acid sequences of SEQ ID NOs 1-20, said method comprising isolating a subfragment nucleic acid sequence from said parent nucleic acid sequence, assaying RNA molecules comprising said subfragment for RBP binding activity or mRNA functionality, and identifying a subfragment nucleic sequence that maintains an RBP binding activity and/or mRNA functionality that is equivalent to said parent sequence.

5. The method of claim 4, wherein said subfragment nucleic acid sequence is isolated by restriction enzyme digestion.

6. The method of claim 4, wherein said subfragment is identified by deletion mapping.

7. The method of claim 4, wherein said mRNA functionality comprises an alteration in pre-mRNA processing or in the stabilization, translational efficiency, localization, sequestration, editing, or splicing functions of said mRNA.

8. A nucleic acid sequence identified as an optimized subfragment of any one of SEQ ID NOs 1-20 by the method of claim 4.

9. A method of identifying a candidate compound having an effect on an RNA/RBP binding pair interaction or mRNA functionality, said method comprising contacting an RNA molecule comprising at least one nucleic acid sequence of any one of SEQ ID NOs 1-20, or at least one optimized subfragment sequence derived from any one of SEQ ID NOs 1-20, with at least one RBP, and at least one test compound, and measuring said RNA/RBP binding pair interaction and/or mRNA functionality, wherein a candidate compound is identified as a test compound that affects said interaction and/or functionality.

10. The method of claim 9, wherein said mRNA functionality comprises an alteration in pre-mRNA processing or in the stabilization, translational efficiency, localization, sequestration, editing, or splicing functions of said mRNA.

11. A method for identifying an RBP that interacts with an RNA molecule comprising the nucleic acid sequence of any one of SEQ ID NOs 1-20, or an optimized subfragment sequence of any one of SEQ ID NOs 1-20, said method

comprising contacting said RNA molecule with at least one RBP, and measuring RNA/RBP binding pair interactions, wherein detection of said interactions identifies said RBP that interacts with said RNA molecule.

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